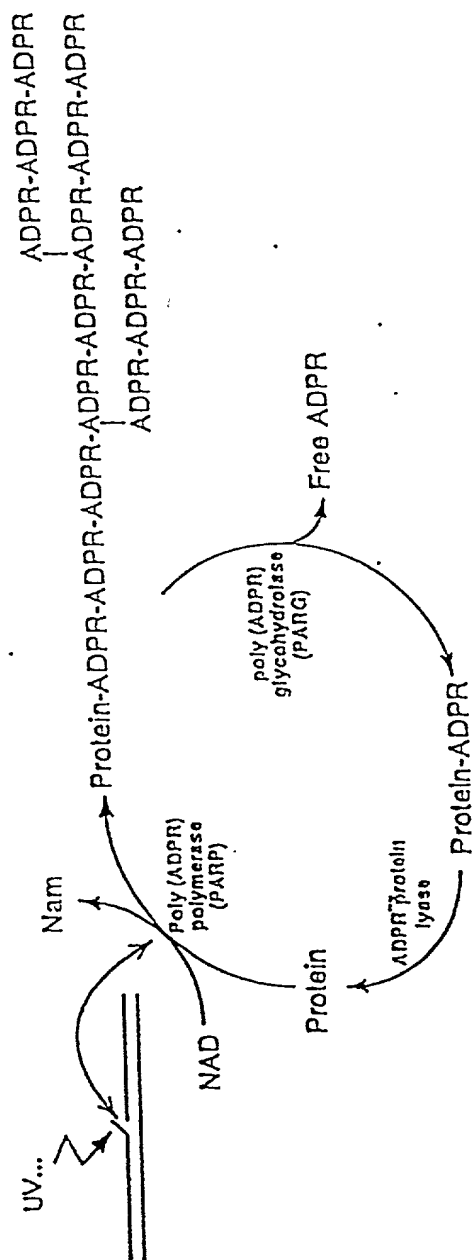
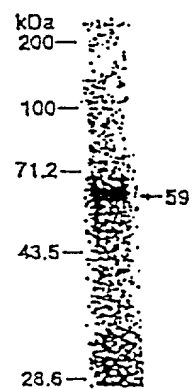


# FIGURE 1



# FIGURE 2



# FIGURE 3

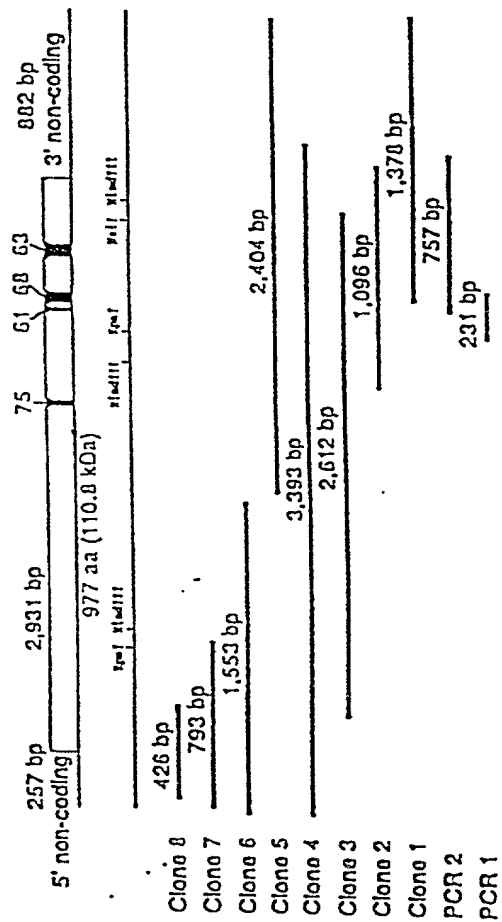
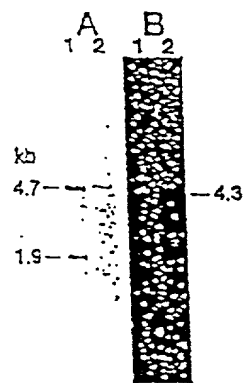


FIGURE 4



# FIGURE 5

bPARG	(422)	ED...	KRKEQCEMKHQ RTE..	RKIPKYIPPH	SEQ ID NO: 19
hPARG	(421)	ED...	RRKEQWETKHQ RTE..	RKIPKYVPPH	SEQ ID NO: 20
mPARG	(413)	ED...	RRKEQCEVRHQ RTE..	RKIPKYIPPN	SEQ ID NO: 21
CePARG	(29)	HQVPTMKRRKL	TEHGNTTESLLKEDPEEPKS		SEQ ID NO: 22
hPARG	(205)	EG...	KRKGD.EVDG.	VDEVAKKSKKEKDK	SEQ ID NO: 23
mPARG	(205)	EG...	KRKGD.EVDG.	TDEVAKKSKRKETDK	SEQ ID NO: 24
bPARG	(208)	EG...	KRKGD.EVDG.	IDVTKKKSKKEKDK	SEQ ID NO: 25
aPARG	(205)	EG...	KRKGE.EVDG..	NVVAKKSKRKEKEK	SEQ ID NO: 26
XIPARG	(204)	EG...	KRKAD.EVDG.	HSAATKKKIKKEKEK	SEQ ID NO: 27
DmPARG	(202)	EELPDTKRAKM.	ELSDTNEEGEKKQR.....		SEQ ID NO: 28
SpPARG	(205)	EGVSSAKKAKI.	EKIDeedAASIKELTEKIKK		SEQ ID NO: 29

FIGURE 6

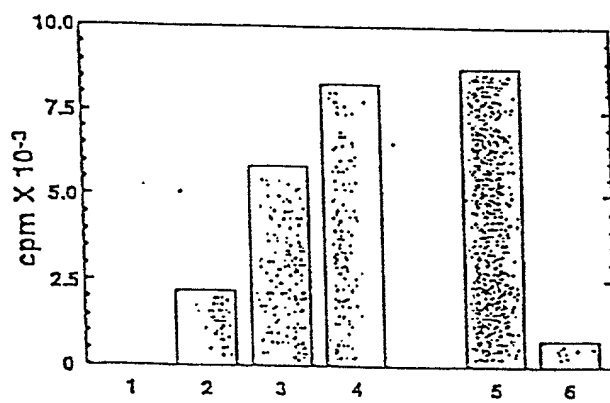


FIGURE 7

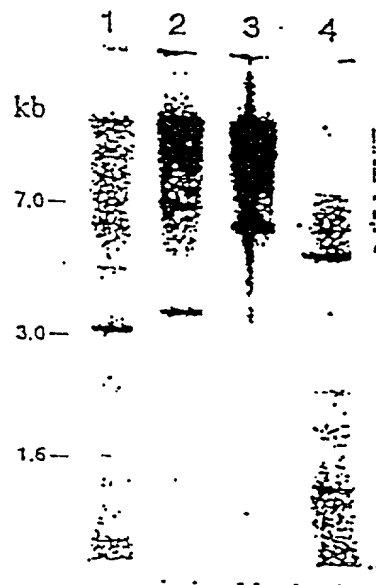


FIGURE 8

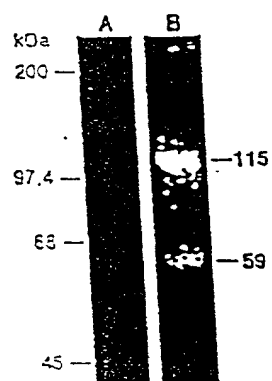




FIGURE 9

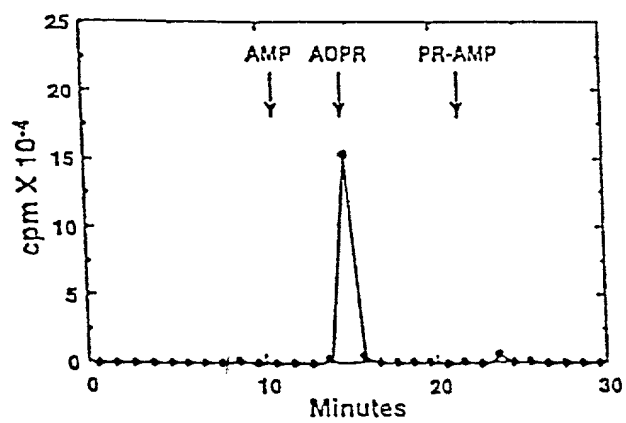
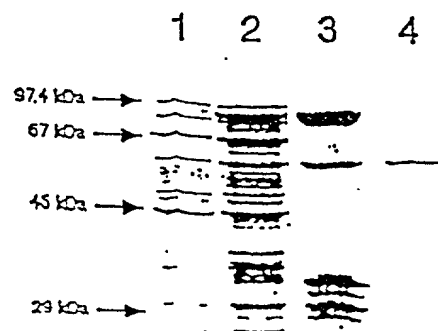


FIGURE 10



# FIGURE 11

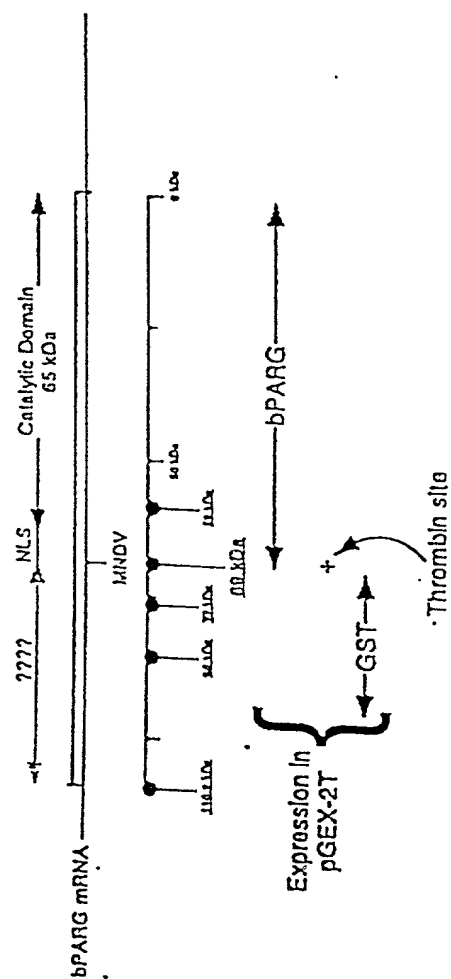


FIGURE 12

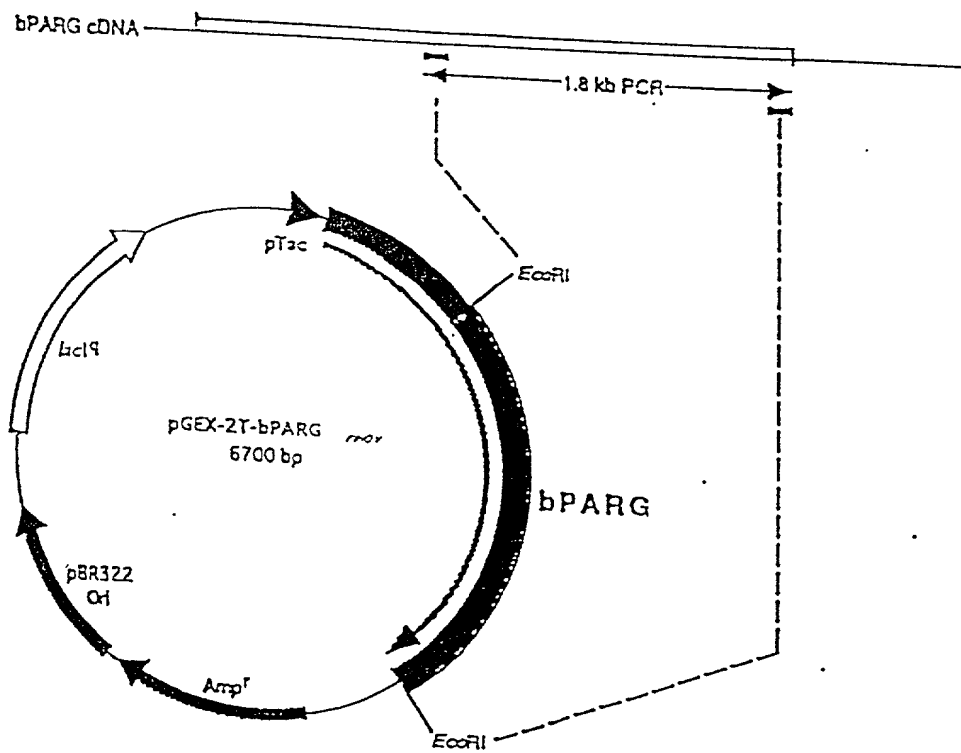


FIGURE 13

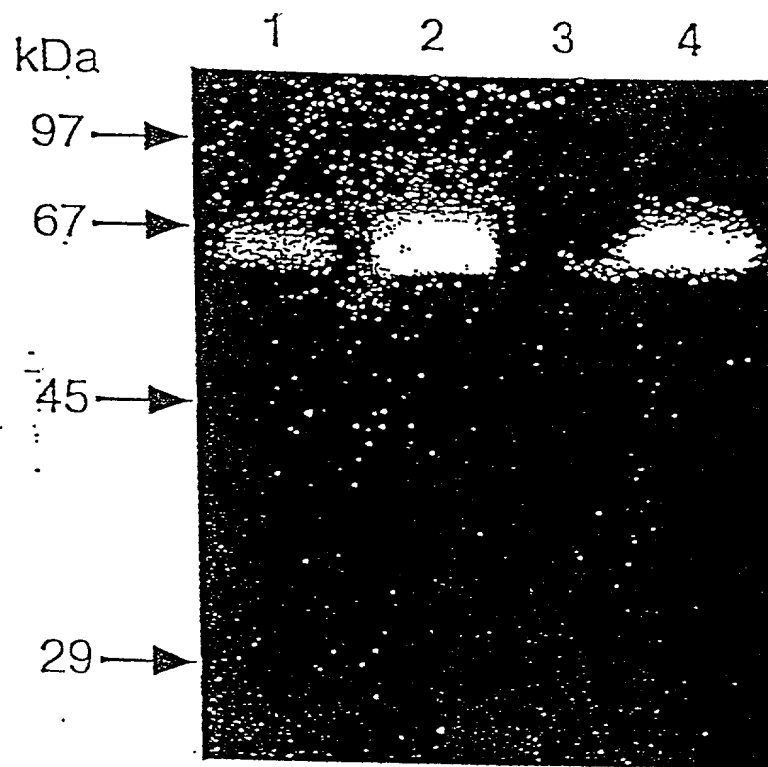


FIGURE 14

## Strategy to Obtain Homologous PARG Sequences

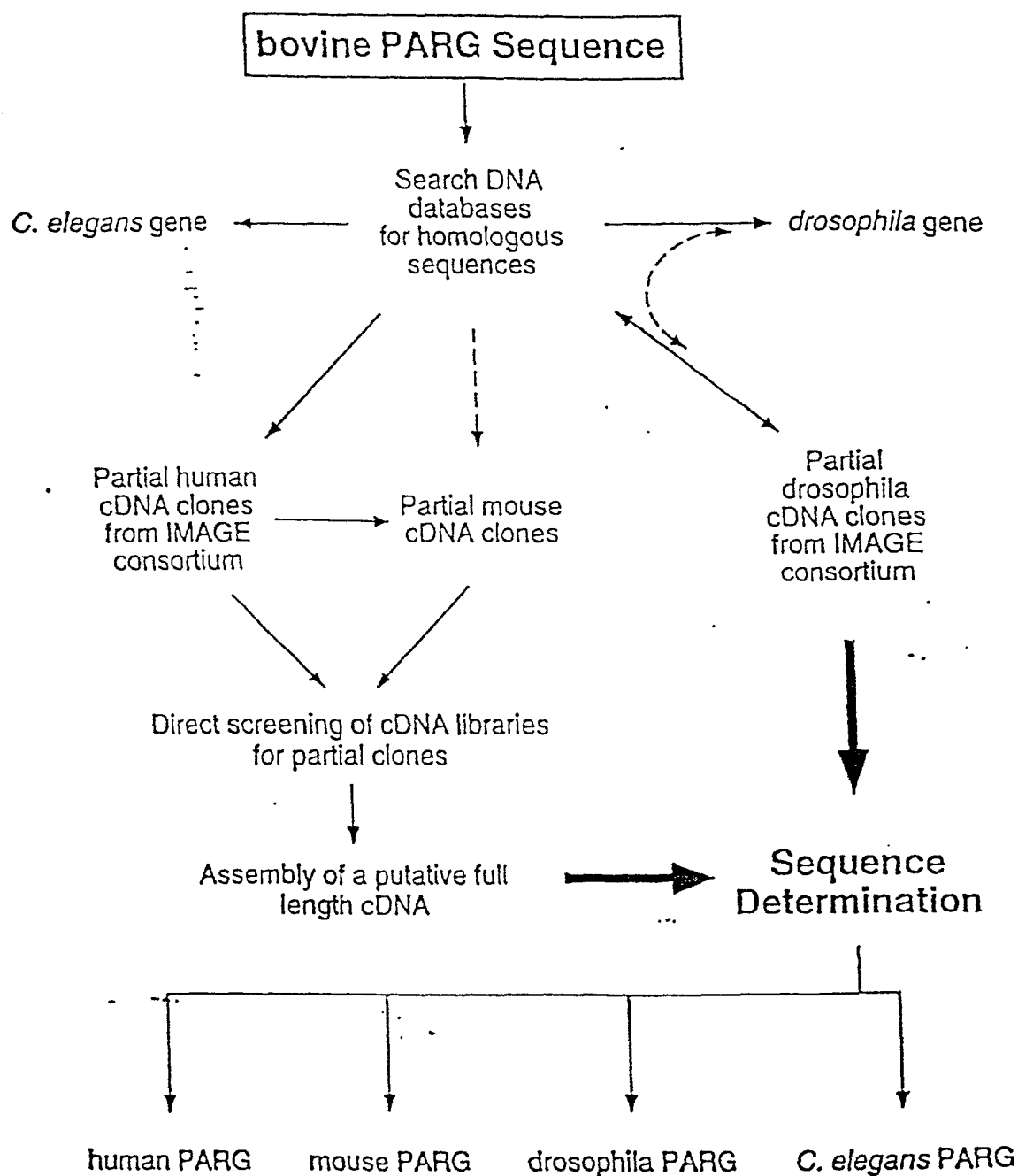
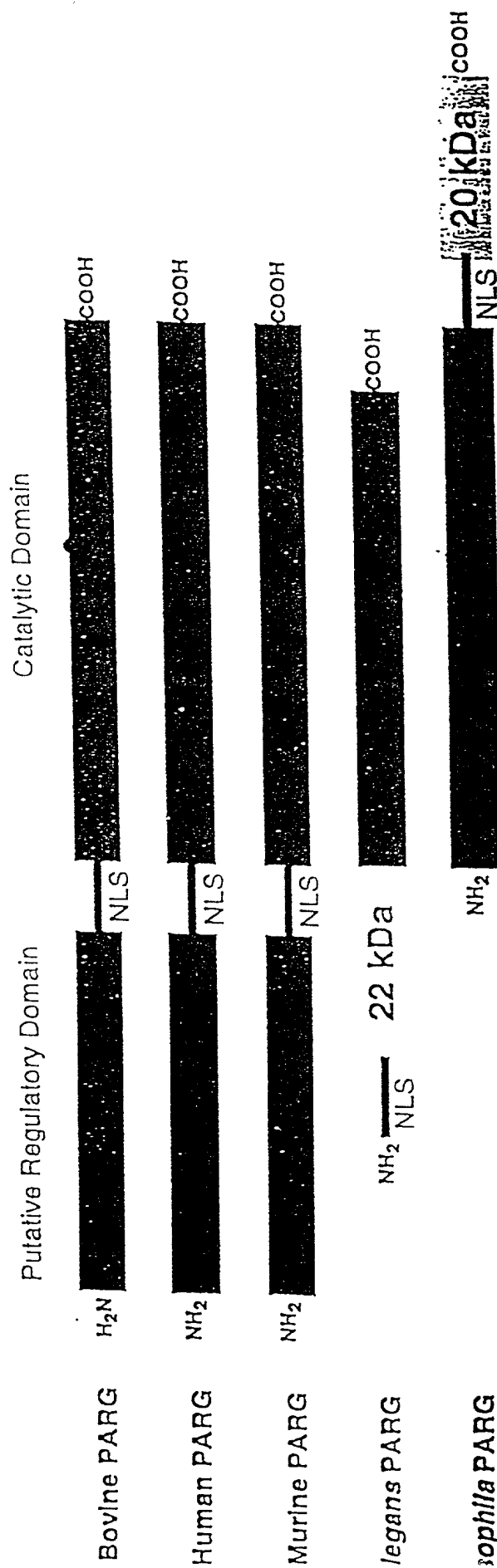


FIGURE 15

# Domain Organization of PARs



# FIGURE 16

## Multiple Alignment of Amino Acid Sequences of PARG from Different Species

```

Bparg 1 MSAGPGCEPCTKRPRWDAATSPPAASDARSFPGRQRRVLDKSDAPVQFRVPPSSSGCALGRAGQHRGSAATSLVFKQKTTITSMWDTKGIXTVESESLSRK
Hparg 1 MNAGPGCEPCTKATRWCAATTS.PAASDARSFPGRQRRVLDKSDAPVQFRVPPSSPACVPGQAGQHRGSAATSLVFKQKTTITSMWDTKGIXTAEESLSLDSK
Mparg 1 MSAGPGWEPCTKA.RWGAAGTSAPTASDSRSFPGRQRRVLDKSDAPVQFRVPPSSPACVSGRAGPHRGHATSFFVFKQKTTITSMWDTKGPKTAESE...SK
Dparg 1
Ceparg 1

Bparg 101 EHHHTREESMSSSVQKDNFIQHNMKLEWVSQLOFDKSPVEKCTQYLKQKQTAAMCKWQNEGPSEERLLESEPPAVTLVPEQFSEANVQSSPKDDSDST
Hparg 100 EHHHTRIESMSSSVQKDNFIQHNMKLEWVSQLOFDKSLTEKSTQILNQKQTAAMCKWQNEGKETEQLLESEPPQTVTLVPEQFSEANVQSSPKDDSDST
Mparg 97 EHHHTRIDSMSSSVQKDNFIQHKVEKLEWVQLNLDKSPTEKSSQILNQKQTAASVCKWQNEGKHAQLLASEPPACTPLPKQLESEANVQSSPETDDSDST
Dparg 1
Ceparg 1 -----MSKKFIELGDPVTDKEDIEDY

Bparg 201 NSEESRDHMQQLTTHVKL...ANAKQTHEDEQGREARSHQKCGKACHFAEACAGCQQETDVSSESPLSDTGSEVDGTGLKXANLNRQESSLGNSPPFFEK
Hparg 200 DSEHRDMQQYLTITVKL...ANAKQTHEDEHAREAKSHQKCSKSCHPGECASCQQDEIDVVPKSPLSVDSGSEVDGTGSKNDKILRQESSLGNSPPFFEK
Mparg 197 DEEDRDHMQQLTPIKL...ANTKPTVGDGQ...ARSNCKSCGSRQSVKDCGTGQQEVDVLPESPLSDVGARDIGTGPKNDKILTGQESSLGNSPPFFEK
Dparg 1
Ceparg 23 VGVGFABQVPTKRRRLTEGHTTESKEDPEEPKSRDVFVSSQSDSESQEDSAENPEIAKEVSENCENLTETLXISNIESLDNVTERSEETLDM...HK

Bparg 298 ESEPESPMDVDNSKNSCQDSSEADESTSPGFDE.QEDSSSAQTANKPSRFPQPREADTELKRRSSAKGGEIRLHPQFEGGESRAGMN.DVNAKRPGSTSSLN
Hparg 297 ESEPESPMDVDNSKNSCQDSSEADESTSPGFDE.QEDSSSAQTANKPSRFPQPREADTELKRRSSAKGGEIRLHPQFEGGESRAGMN.DVNAKRPGSTSSLN
Mparg 291 ESEPESPMDVDNSKNSCQDSSEADESTSPGFDE.QEDSSSAQTANKPSRFPQPREADTELKRRSSAKGGEIRLHPQFEGGESRAGMN.DVNAKRPGSTSSLN
Dparg 1
Ceparg 119 STEPMEE.DVNNKSHIDVAINSDDEDELVLBENNEKMRDGEQVQQLS..QDLFADDQELIEYFGIMKDDTTIQLDITSEVETAQKMEIETADSTFVG

Bparg 396 VECRNSKQHGKRDSDKITDEFMRVPAEDKRKEQCEMKXQRTERRKIPKIYPPHLSPOKKMLGTPIEM...RRMPRCGIRLPLRPSANHTVIRVDLLRIG
Hparg 395 VECRNSKQHGKRDSDKITDELMLRPAEDRRKEQWETKQRTERRKIPKIYPPHLSPOKKMLGTPIEM...RRMPRCGIRLPLRPSANHTVIRVDLLRIG
Mparg 387 VECRNSKQHGKRDSDKITDEFMRVPAEDKRKEQCEMKXQRTERRKIPKIYPPHLSPOKKMLGTPIEM...RRMPRCGIRLPLRPSANHTVIRVDLLRIG
Dparg 32 .....TNRLGK...ALCLYCARMSKSPDGGCISIE...TREE.PENLANSL...DSDVRGVSKHAIRHRQPPFELENLPVTAGNLRVNIQLPIRET.
Ceparg 216 EDSKATKTVRTSSSSP...LSVSTCEAPAKGRARMIQKELEKXVIAFTEGNLT...LQPDNLKVDPDNRMYR.CTIPNFPASQ...KLRED.WRIG

Bparg 494 EVFK.PPPTHFKDLMDNKEVXKPCSEQNLIPVEDENGE.RAAGSRWELIQTALLNRLRTPQNLKDAILKXNVAYSKKWDF TALIDFMDKVLBEEAAQELI
Hparg 493 EVFK.PPPTHFKDLMDNKEVXKPCSEQNLIPVEDENGE.RAAGSRWELIQTALLNRLRTPQNLKDAILKXNVAYSKKWDF TALIDFMDKVLBEEAAQELI
Mparg 485 EVFK.PPPTHFKDLMDNKEVXKPCSEQNLIPVEDENGE.RAAGSRWELIQTALLNRLRTPQNLKDAILKXNVAYSKKWDF TALIDFMDKVLBEEAAQELI
Dparg 115 .PPR.PIKSPGX..WDSEVRLPCAPESKIPRENPDGS.TTDFRWNIERALLQPIKTCEELOAAIISNTTIRQWEPFALHQLLDEELEDSETRVFP
Ceparg 303 ..PKIVLPQRWR.RFDSRGR...RDSFTYFKRKLQDILKCIKTYTGYFMVGLLE.....HWE..FDPDITYK...LPAL.EMYIKEMSELVGREEV

Bparg 592 QSILPDMVKIALCLPNICTQPIPLLKQKMMHSITMSQEQIASLLANAFCTFPRRNA.KMKSEYSSYPDINFNRLPFGRSSRKPEKLTLPFCYFRRV..T
Hparg 591 QSILPDMVKIALCLPNICTQPIPLLKQKMMHSITMSQEQIASLLANAFCTFPRRNA.KMKSEYSSYPDINFNRLPFGRSSRKPEKLTLPFCYFRRV..T
Mparg 583 QSILPDMVKIALCLPNICTQPIPLLKQKMMHSITMSQEQIASLLANAFCTFPRRNA.KMKSEYSSYPDINFNRLPFGRSSRKPEKLTLPFCYFRRV..T
Dparg 210 EDLLPRIIRLALRLPDLIQSPVPLKHEKNASLSLSQQQISCLLANAFCTFPRNTLKRKSEISTFPDINFNRLYQSTGPAVLEKLEKIMHYFRRYCP
Ceparg 384 LEKPARVARIKTAEDILPERIIRLVGDVE.BATLSHXCAALVARMFFA.....RPDSPPS.....PCRILSSDKSICVEKLF7LFTIF.....

Bparg 689 EKK...PTGLVTFIRQS.L.ED.F.PEWERCEKLL..TRLHVITEGTIEGNGGQMLQVDFANRFVGGGVISAGLVQEEIRFLINPELIVSRLFTVLDH
Hparg 688 EKK...PTGLVTFIRQS.L.ED.F.PEWERCEKPL..TRLHVITEGTIEGNGGQMLQVDFANRFVGGGVISAGLVQEEIRFLINPELIVSRLFTVLDH
Mparg 680 EKK...PTGLVTFIRQS.L.ED.F.PEWERCEKPL..TRLHVITEGTIEGNGGQMLQVDFANRFVGGGVISAGLVQEEIRFLINPELIVSRLFTVLDH
Dparg 310 ERDASNVPTGVVTFVRRSGLPEH.L.IDMSQSAAPLGDVPLEHVDACOTIEDEGICGLQVDFANKILGGGVLGCGVQEEIRFVICPELLVGKLYTECLRP
Ceparg 463 DKMSHDPDPAVSYF.RLTFMDKDTFNEEM.KDKXLRSLRBEVFFDEMLIEDTAL.CTQVDFANEHLGGGVLEHSGSVQEEIRFLMCPKEMVGMGLLCEKMKQ

Bparg 779 NECLIIITGTEQISEYTGIAETIRWA....RSHEDRSE.RDDMQRRTEIVAIDALEFR.RYLD...QFVPEKIRRELKAYCGFLRPGVSSSENLASA
Hparg 778 NECLIIITGTEQISEYTGIAETIRWS....RSHEDGSE.RDDCERRCTEIVAIDALEFR.RYLD...QFVPEKIRRELKAYCGFLRPGVSSSENLASA
Mparg 770 NECLIIITGTEQISEYTGIAETIRWA....RSHEDGSE.RDDMQRRCTEIVAIDALEFR.RYLD...QFVPEKIRRELKAYCGFLRPGVSSSENLASA
Dparg 408 FEALVHLGAERYISNITGIAGSPENS....GNFEDSTP.RDSSGRRQTAIVAIDALEFA.QSHH...QIREDLMERELNKAIIGFVHNMVTPP..PGVA
Ceparg 560 LEAISIVGAIYFSSITGICETLKMAELQPNHSRQNTNEFRDGRGLRVETIATIDALFKGSKLDCQTEQLNKANIIREMKKASIGFMSQCPKFTIP.IV

Bparg 668 TGNWGGCAFGGDARLKALIQILAAAAAERDVVIFTPGDSLMRDIYSMTFLTERKLTVDG.VIKLLLRINIENECRNCSTPGP.....DIKLYPPIIYA
Hparg 667 TGNWGGCAFGGDARLKALIQILAAAAAERDVVIFTPGDSLMRDIYSMTFLTERKLTVDG.VIKLLLRINIENECRNCSTPGP.....DIKLYPPIIYA
Mparg 659 TGNWGGCAFGGDARLKALIQILAAAAAERDVVIFTPGDSLMRDIYSMTFLTERKLTVDG.VIKLLLRINIENECRNCSTPGP.....DIKLYPPIIYA
Dparg 495 TGNWGGCAFGGDSILKALLQMLVCAQLGRPLATYTFGNVFERDDPEHMLLFRNDGTTVQQ.LWS.ILRYSRLIKEKSSKEPRENKASKKLYDI...
Ceparg 659 TGNWGGCAFGNGDXPLKFIQVIAAGVADRPLHFCSGPEPLAACKKIIERMKQKDVTLGKSCFSIFS-----

Bparg 961 VESCTQTTNQPGQRTGA-----
Hparg 960 VESCAETADHSGQRTGT-----
Mparg 952 VESSAETDMKPGQKACT-----
Dparg 590 KEELKKVRDVPCEGASAZAGSSRVAGLGEGKSETSAKSSPELNKQPARPQITITQSTDLLPAQLSQDNHSSSEDQALLHLSDDDEANAMKEAASLEAKS
Ceparg 727 -----

Bparg 978 -----
Hparg 977 -----
Mparg 969 -----
Dparg 690 SVEISNSSTTSKTSSTATKSMGSGGRQLSLLHMLDTHIEKGSASKRPRKSPNCSKAEGSAKSRKEIDVTDKDEKDDIVD
Ceparg 727 -----

```



FIGURE 17

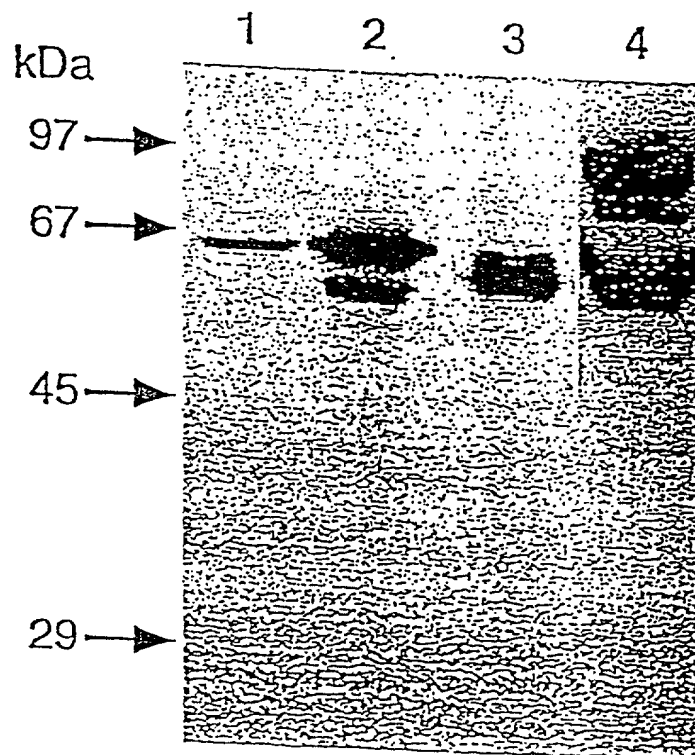
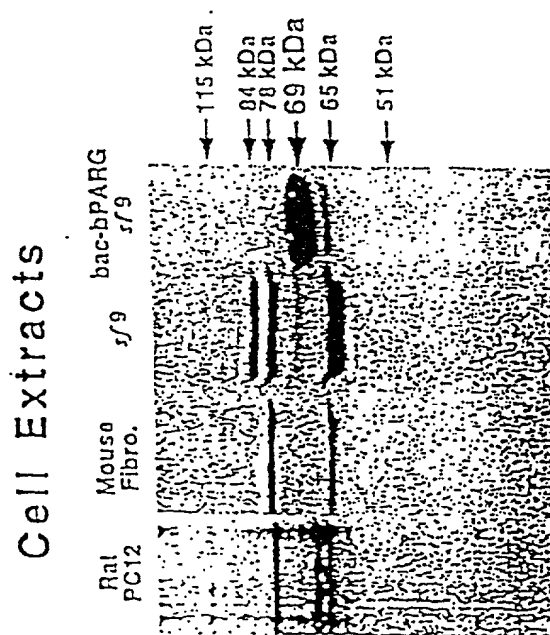


FIGURE 18

B



A

Bovine Tissue

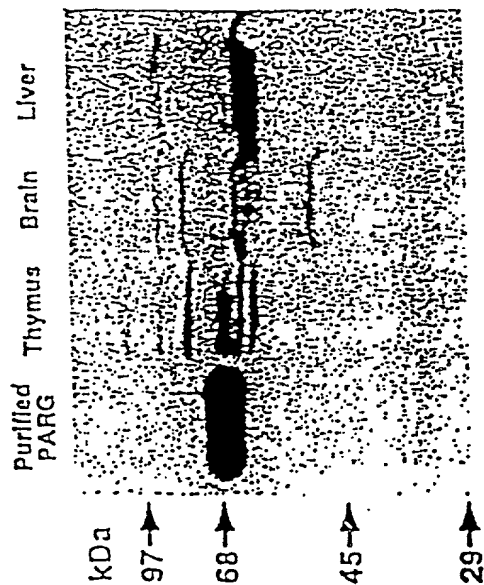
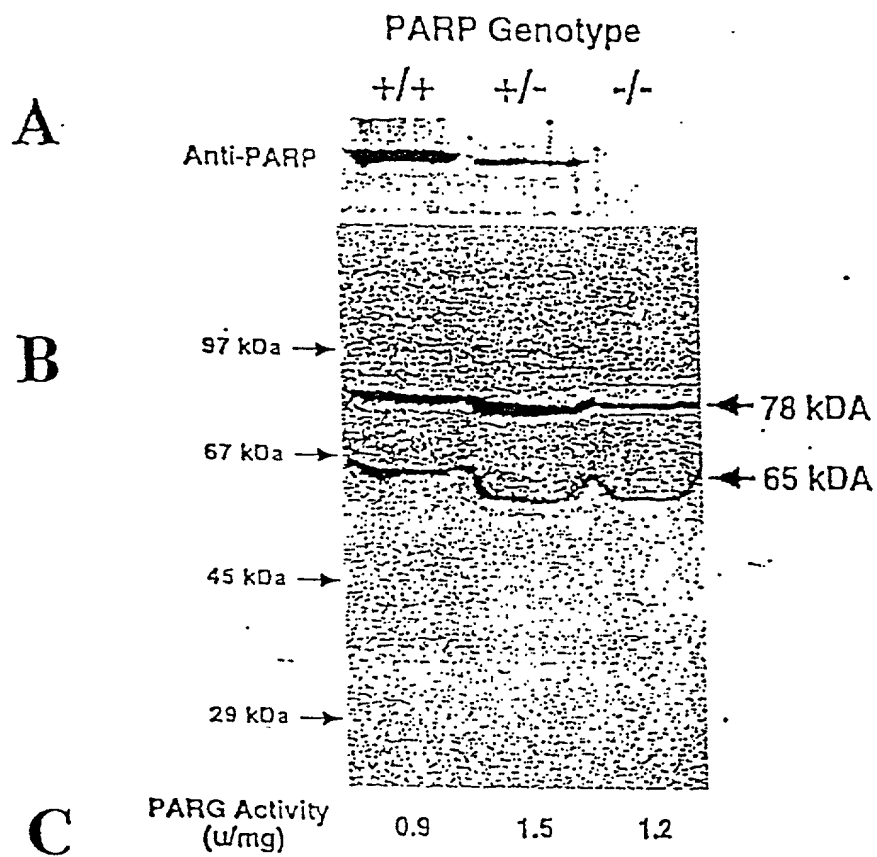
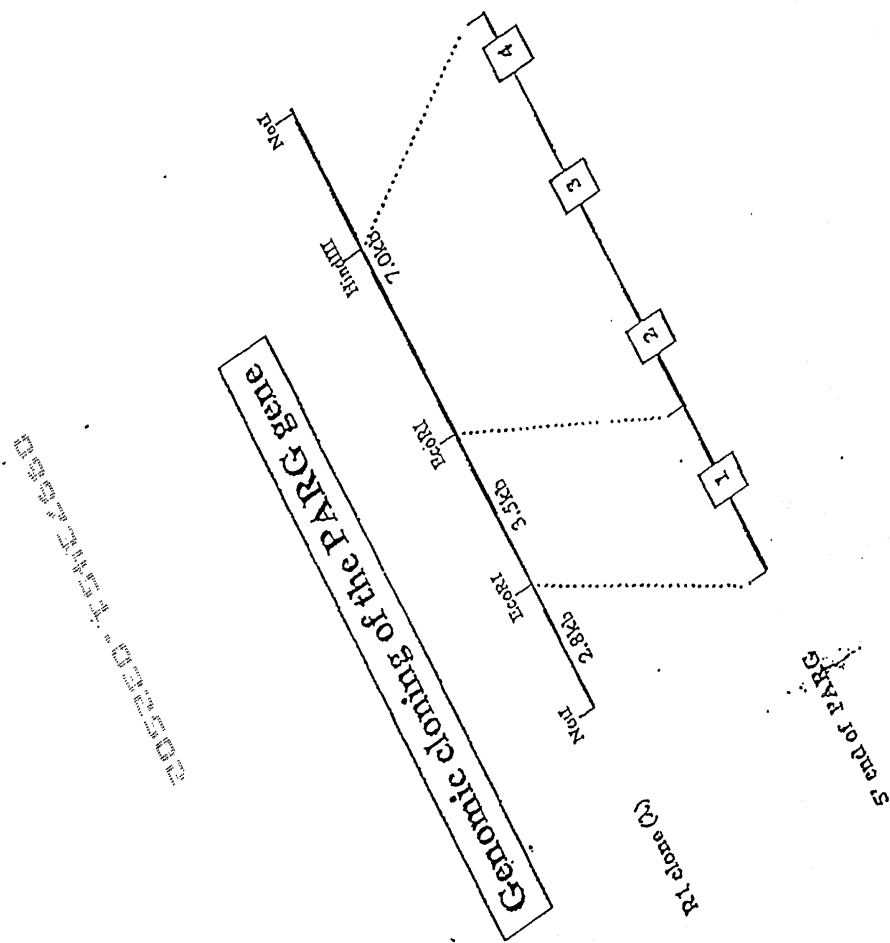


FIGURE 19



**FIGURE 20**



**FIGURE 21** 44650

